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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Wed Jun 27 16:17:41 EDT 2007

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Application No: 10505183 Version No: 2.0

Input Set:

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Finished: 2007-06-26 17:13:54.020
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 832 ms
Total Warnings: 14
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

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<110> Negishi et al.

<120> Mutated constitutively active nuclear orphan receptor

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<141> 2004-08-18

<150> PCT/US03/05163

<151> 2003-02-19

<150> US 60/358,500

<151> 2002-02-19

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cctgctgcct aagggaaca ggagacc atg aca gct atg cta aca cta gaa acc 174
Met Thr Ala Met Leu Thr Leu Glu Thr
1 5
atg gcc agt gaa gaa gaa tat ggg ccg agg aac tgt gtg gtg tgt gga 222
Met Ala Ser Glu Glu Tyr Gly Pro Arg Asn Cys Val Val Cys Gly
10 15 20 25
gac cgg gcc aca ggc tat cat ttc cac gcc ctg act tgt gag ggc tgc 270
Asp Arg Ala Thr Gly Tyr His Phe His Ala Leu Thr Cys Glu Gly Cys
30 35 40
aag ggc ttc ttc aga cga aca gtc agc aaa acc att ggt ccc atc tgt 318
Lys Gly Phe Phe Arg Arg Thr Val Ser Lys Thr Ile Gly Pro Ile Cys
45 50 55
ccg ttt gct gga agg tgt gag gtc agc aag gcc cag aga cgc cac tgt 366
Pro Phe Ala Gly Arg Cys Glu Val Ser Lys Ala Gln Arg Arg His Cys
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cca gcc tgc agg ttg cag aag tgt cta aat gtt ggc atg agg aaa gac 414
Pro Ala Cys Arg Leu Gln Lys Cys Leu Asn Val Gly Met Arg Lys Asp

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Met Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Arg Gln Ala			
90	95	100	105
cag cgg cgg gca gag aaa gca tct ttg caa ctg aat cag cag cag aaa			510
Gln Arg Arg Ala Glu Lys Ala Ser Leu Gln Leu Asn Gln Gln Gln Lys			
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gaa ctg gtc cag atc ctc ctg ggg gcc cac act cgc cat gtg ggc cca			558
Glu Leu Val Gln Ile Leu Leu Gly Ala His Thr Arg His Val Gly Pro			
125	130	135	
ttg ttt gac cag ttt gtg cag ttc aag cct cca gcc tat ctg ttc atg			606
Leu Phe Asp Gln Phe Val Gln Phe Lys Pro Pro Ala Tyr Leu Phe Met			
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cat cac cgg cct ttc cag cct cgg ggc ccc gtg ttg cct ctg ctc aca			654
His His Arg Pro Phe Gln Pro Arg Gly Pro Val Leu Pro Leu Leu Thr			
155	160	165	
cac ttt gca gat atc aac acg ttt atg gtg caa cag atc atc aag ttc			702
His Phe Ala Asp Ile Asn Thr Phe Met Val Gln Gln Ile Ile Lys Phe			
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acc aag gat ctg ccg ctc ttc cgg tcc cta acc atg gag gac cag atc			750
Thr Lys Asp Leu Pro Leu Phe Arg Ser Leu Thr Met Glu Asp Gln Ile			
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tcc ctt ctc aag gga gcg gct gtg gaa ata ttg cat atc tca ctc aac			798
Ser Leu Leu Lys Gly Ala Ala Val Glu Ile Leu His Ile Ser Leu Asn			
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Thr Thr Phe Cys Leu Gln Thr Glu Asn Phe Phe Cys Gly Pro Leu Cys			
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tac aag atg gag gac gca gtc cat gca ggg ttc cag tac gag ttt ttg			894
Tyr Lys Met Glu Asp Ala Val His Ala Gly Phe Gln Tyr Glu Phe Leu			
235	240	245	
gag tcg atc ctc cac ttc cat aaa aac ctg aaa gga ctg cat ctc cag			942
Glu Ser Ile Leu His Phe His Lys Asn Leu Lys Gly Leu His Leu Gln			
250	255	260	265
gag cct gag tat gtg ctc atg gct gcc acg gcc ctc ttc tcc cct gac			990
Glu Pro Glu Tyr Val Leu Met Ala Ala Thr Ala Leu Phe Ser Pro Asp			
270	275	280	
aga ccc gga gtt acc caa aga gaa gag ata gat cag cta caa gag gag			1038
Arg Pro Gly Val Thr Gln Arg Glu Glu Ile Asp Gln Leu Gln Glu Glu			
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atg gcg ctg att ctg aac aac cac att atg gaa caa cag tct cgg ctc			1086
Met Ala Leu Ile Leu Asn Asn His Ile Met Glu Gln Gln Ser Arg Leu			
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caa agt cgg ttt ctg tat gca aag ctg atg ggc ctg ctg gct gac ctc	1134
Gln Ser Arg Phe Leu Tyr Ala Lys Leu Met Gly Leu Leu Ala Asp Leu	
315 320 325	

cgg agt ata aac aat gca tac tcc tat gaa ctt cag cgc ttg gag gaa	1182
Arg Ser Ile Asn Asn Ala Tyr Ser Tyr Glu Leu Gln Arg Leu Glu Glu	
330 335 340 345	

ctg tct gct atg acg ccg ctg ctc ggg gag att tgc agt tga	1224
Leu Ser Ala Met Thr Pro Leu Leu Gly Glu Ile Cys Ser	
350 355	

ggcccaggct tgcataccttt cccagacccc ccagggatac actggcctgg aaagggtaca	1284
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acagtc	1350
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Phe His Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
35 40 45

Val Ser Lys Thr Ile Gly Pro Ile Cys Pro Phe Ala Gly Arg Cys Glu
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Val Ser Lys Ala Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys
65 70 75 80

Cys Leu Asn Val Gly Met Arg Lys Asp Met Ile Leu Ser Ala Glu Ala
85 90 95

Leu Ala Leu Arg Arg Ala Arg Gln Ala Gln Arg Arg Ala Glu Lys Ala
100 105 110

Ser Leu Gln Leu Asn Gln Gln Gln Lys Glu Leu Val Gln Ile Leu Leu
115 120 125

Gly Ala His Thr Arg His Val Gly Pro Leu Phe Asp Gln Phe Val Gln
130 135 140

Phe Lys Pro Pro Ala Tyr Leu Phe Met His His Arg Pro Phe Gln Pro
145 150 155 160

Arg Gly Pro Val Leu Pro Leu Leu Thr His Phe Ala Asp Ile Asn Thr
165 170 175

Phe Met Val Gln Gln Ile Ile Lys Phe Thr Lys Asp Leu Pro Leu Phe
180 185 190

Arg Ser Leu Thr Met Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala
195 200 205

Val Glu Ile Leu His Ile Ser Leu Asn Thr Thr Phe Cys Leu Gln Thr
210 215 220

Glu Asn Phe Phe Cys Gly Pro Leu Cys Tyr Lys Met Glu Asp Ala Val
225 230 235 240

His Ala Gly Phe Gln Tyr Glu Phe Leu Glu Ser Ile Leu His Phe His
245 250 255

Lys Asn Leu Lys Gly Leu His Leu Gln Glu Pro Glu Tyr Val Leu Met
260 265 270

Ala Ala Thr Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg
275 280 285

Glu Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Ile Leu Asn Asn
290 295 300

His Ile Met Glu Gln Gln Ser Arg Leu Gln Ser Arg Phe Leu Tyr Ala
305 310 315 320

Lys Leu Met Gly Leu Leu Ala Asp Leu Arg Ser Ile Asn Asn Ala Tyr
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tccaatcact ggcaactcct gagatcagag gaaaaccagc aacagcgtgg gagtttgggg 180

agaggcattc cataccagat tctgtggcct gcaggtgaca tgctgcctaa gagaagcagg 240

agtctgtgac agccacccca acacgtgacg tc atg gcc agt agg gaa gat gag 293
Met Ala Ser Arg Glu Asp Glu
1 5

ctg agg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt 341
Leu Arg Asn Cys Val Val Cys Gly Asp Gln Ala Thr Gly Tyr His Phe
10 15 20

aat gcg ctg act tgt gag ggc tgc aag ggt ttc ttc agg aga aca gtc 389
Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val
25 30 35

agc aaa agc att ggt ccc acc tgc ccc ttt gct gga agc tgt gaa gtc 437
Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val
40 45 50 55

agc aag act cag agg cgc cac tgc cca gcc tgc agg ttg cag aag tgc 485
Ser Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys
60 65 70

tta gat gct ggc atg agg aaa gac atg ata ctg tcg gca gaa gcc ctg 533
Leu Asp Ala Gly Met Arg Lys Asp Met Ile Leu Ser Ala Glu Ala Leu
75 80 85

gca ttg cgg cga gca aag cag gcc cag cgg cgg gca cag caa aca cct 581
Ala Leu Arg Arg Ala Lys Gln Ala Gln Arg Arg Ala Gln Gln Thr Pro
90 95 100

gtg caa ctg agt aag gag caa gaa gag ctg atc cgg aca ctc ctg ggg 629
Val Gln Leu Ser Lys Glu Gln Glu Glu Leu Ile Arg Thr Leu Leu Gly
105 110 115

gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag ttt 677

Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln Phe	
120 125 130 135	
agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc ctg	725
Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr Leu	
140 145 150	
gcc cct gtg ctg cct ctg gtc aca cac ttc gca gac atc aac act ttc	773
Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr Phe	
155 160 165	
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Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe Arg	
170 175 180	
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Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala Val	
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Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr Gln	
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Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala Arg	
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Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His Gly	
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265 270 275	
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Gln Glu Ile Cys Ser	

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